

AP20 Rec'd PCT/PTO 14 JUL 2006

<110> Korea Research Institute of Bioscience and Biotechnology  
 <120> Rapid screening method of translational fusion partners for  
 producing recombinant proteins and translational fusion partners  
 screened therefrom

<150> KR10-2004-0003957

<151> 2004-01-19

<160> 45

<170> Kopatentin 1.71

<210> 1

<211> 105

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> PEPTIDE

<222> (1)..(105)

<223> TFP1

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 1 5 10 15

Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser  
 20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala  
 35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro  
 50 55 60

Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Ile Ala  
 65 70 75 80

Thr Glu Ala Val Glu Val Ala Ala Gly Gly Lys Leu Thr Leu Leu Asp  
 85 90 95

Gly Glu Lys Tyr Val Phe Ser Ser Asp  
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<212> DNA

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<220>

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<223> TFP1

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 tactattttct ttctttttat tggtaaactc tcgcccatta caaaaaaaaa agagatgttc 120  
 aatcgtttta acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180  
 ggtgactctt acaccaatag cacctctctc gcagacttga gtctatcac ttccgtctcg 240  
 tcagctagtg caagtggccac cgcttccgac tcactttctt ccagtgcagg taccgtttat 300  
 ttgccatcca caacaattag cggtgatctc acagttactg gtaaagtaat tgcaaccgag 360  
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 tcatctgac 430

<210> 3

<211> 117

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<212> PRT  
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<220>  
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 Val Ser Ala Leu Gln Val Asn Asn Ser Cys Val Ala Phe Pro Pro Ser  
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 Asn Leu Arg Gly Lys Asn Gly Asp Gly Thr Asn Glu Gln Tyr Ala Thr  
 35 40 45  
 Ala Leu Leu Ser Ile Pro Trp Asn Gly Pro Pro Glu Ser Leu Arg Asp  
 50 55 60  
 Ile Asn Leu Ile Glu Leu Glu Pro Gln Val Ala Leu Tyr Leu Leu Glu  
 65 70 75 80  
 Asn Tyr Ile Asn His Tyr Tyr Asn Thr Thr Arg Asp Asn Lys Cys Pro  
 85 90 95  
 Asn Asn His Tyr Leu Met Gly Gly Gln Leu Gly Ser Ser Ser Asp Asn  
 100 105 110  
 Arg Ser Leu Asn Asp  
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<210> 4  
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 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> gene  
 <222> (1)..(424)  
 <223> TFP2

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 gtgagcgacc tccaggtaaa caattcatgt gtcgcttttc cgccatcaaa tctcagaggg 180  
 aaaaatggag acggtactaa tgaacagtat gcaactgcac tactttctat tccctggaat 240  
 ggaccicctg agtcattgag ggatattaat cttattgaac tcgaaccgca agttgcactc 300  
 tatttgctcg aaaattatat taaccattac tacaacacca caagagacaa taagtgcctt 360  
 aataaccact acctaatggg agggcagttg ggtagctcat cggataatag gatttgaac 420  
 gatc 424

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                   20                  25                  30  
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr  
                   35                  40                  45  
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg  
                   50                  55                  60  
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala  
                   65                  70                  75                  80  
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala  
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                   100

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 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> gene  
 <222> (1)..(642)  
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 acgtccacaa acaaaaacaa aaataagaaa taggttgaca gtgggtgaaa aattctcgaa 180  
 gggttcatct ccaaacagtc agtatataag tattcgggaa agagagccaa tctatcttgt 240  
 gggtgggtcia tcttaacctt ctctttttgg cagtagtaat tglaaatcaa gacacataaa 300  
 actattttac tcgctaaact tacatctaaa atgcaattca aaaacgtcgc cctagctgcc 360  
 tccgttgctg ctctatccgc cactgcttct gctgaagggt acactccagg tgaacctgg 420  
 tccaccttaa cccaacccg ctccatctct tgtgggtgct cgaatacac taccaccttt 480  
 gggtatgctg ttcaagctat tacctcttca aaagctaaga gagacgttat ctctcaaatt 540  
 ggtagcggtc aagtccaagc cacttctgct gctactgctc aagccaccga tagtcaagcc 600  
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<210> 7  
 <211> 50  
 <212> PRT  
 <213> *Hansenula polymorpha*

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 <222> (1)..(50)  
 <223> TFP4

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                   20                  25                  30  
 Gln Met Lys Glu Arg Phe Thr Thr Glu Lys Leu Cys Ala Leu Asp Asp  
                   35                  40                  45  
 Lys Ile  
           50

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<210> 8  
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 <212> DNA  
 <213> Hansenula polymorpha

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 <221> gene  
 <222> (1)..(179)  
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 ccacgtagg cggggggatg gctgcaccgg ttgagtctct ggccgggacc caacggtatc 120  
 tggtgcaaat gaaggagcgg ttcaccacag agaagctgtg tgctttggac gacaagatc 179

<210> 9  
 <211> 71  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<220>  
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 <222> (1)..(71)  
 <223> TFP1-3

<400> 9  
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 1 5 10 15  
 Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser  
 20 25 30  
 Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala  
 35 40 45  
 Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro  
 50 55 60  
 Ser Thr Thr Ile Ser Gly Asp  
 65 70

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<220>  
 <221> gene  
 <222> (1)..(329)  
 <223> TFP1-4

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 cgcggcgctc tcggtgactc ttacaccaat agcacctcct ccgcagactt gagttctatc 120  
 acttcgctct cgtcagctag tgcaagtgcc accgcttcgg actcacttc ttccagtgac 180  
 ggtaccgttt atttgccatc cacaacaatt agcggtgatc tcacagttac tggtaaagta 240  
 attgaaccg aggcctgga agtcgctgcc ggtgtaagt tgactttact tgacggtgaa 300  
 aaatacgtct tctcatctga tctctaga 329

<210> 11  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> JH97(Sfi-HSA-forward primer)

<400> 11  
ccggccatta cggccgtgat gcacacaaga gtgag 35

<210> 12  
<211> 29  
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<220>  
<223> JH119(Sfi-HSA-reverse primer)

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ccggccgagg cggcctaagc ctaaggcag 29

<210> 13  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> JH99(Sfi-INV-forward primer)

<400> 13  
gggcggccgc ctggcccta gataaaaggc caatgacaaa cgaaactagc 50

<210> 14  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> JH100(SalI-INV-reverse primer)

<400> 14  
ccgtcgactt actatittac ttcccttact tg 32

<210> 15  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> JH106(Sfi-IL2-forward primer)

<400> 15  
gcggccatta cggccgtgca cctacttcaa gtctctac 37

<210> 16  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> JH107(Sfi-IL2-reverse primer)

<400> 16  
gcggccatta cggccgtgca cctacttcaa gtctctac 37

<210> 17  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> JH120(BamHI-IL2-1-forward primer)

<400> 17  
cgggatccgc acctacttica agttct 26

<210> 18  
<211> 27  
<212> DNA  
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<220>  
<223> JH121(BamHI-IL2-2-forward primer)

<400> 18  
cgggatcctg cacctacttc aagttct 27

<210> 19  
<211> 28  
<212> DNA  
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<220>  
<223> JH122(BamHI-IL2-3-forward primer)

<400> 19  
cgggatcctt gcacctactt caagttct 28

<210> 20  
<211> 22  
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<220>  
<223> JH123(INV-1-reverse primer)

<400> 20  
ccattgaagg aaccaacaaa at 22

<210> 21  
<211> 22  
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<223> JH124(INV-forward primer)

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<210> 22  
<211> 29  
<212> DNA  
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<220>  
<223> JH95(INV-2-reverse primer)

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ggctcgagct attttacttc ccttacttg 29

<210> 23  
<211> 23  
<212> DNA  
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<220>  
<223> JH132(SacI-GAL-forward primer)

<400> 23  
gggagctcat cgcttcgctg att 23

<210> 24  
<211> 27  
<212> DNA  
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<220>  
<223> JH137(IL-2-Term-reverse primer)

<400> 24  
ccgtcgactt aagttagtgt tgagatg 27

<210> 25  
<211> 47  
<212> DNA  
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<220>  
<223> HY22(TFP1-LDKR-reverse primer)

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<210> 26  
<211> 46  
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<220>  
<223> HY23(TFP1-LDKR-forward primer)

<400> 26  
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<210> 27  
<211> 46  
<212> DNA  
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<220>  
<223> HY20(TFP2-LDKR-reverse primer)

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<210> 28  
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<220>  
<223> HY21(TFP2-LDKR-forward primer)

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ggagtttgaa cgatcctcta gataaaaggg cacctacttc aagttc 46

<210> 29  
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<220>  
<223> HY24(TFP4-LDKR-reverse primer)

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gaacttgaag taggtgccct tttatcaagg atcttgcgt ccaaagc 47

<210> 30  
<211> 47  
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<220>  
<223> HY25(TFP4-LDKR-forward primer)

<400> 30  
gctttggaag acaagatcct tgataaaagg gcacctactt caagttc 47

<210> 31  
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<220>  
<223> JH143(XbaI-TFP1-d-reverse primer)

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<210> 32  
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<223> JH142(XbaI-TFP1-c-reverse primer)

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<210> 33  
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<220>  
<223> JH141(XbaI-TFP1-b-reverse primer)

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<210> 34  
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<212> DNA  
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<220>  
<223> JH140(SpeI-XbaI-LDKR-forward primer)

<400> 34  
ggactagtct agataaaagg gcacc 25

<210> 35  
<211> 42  
<212> DNA  
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&lt;220&gt;

&lt;223&gt; HY38(TFP1-UTR-forward primer)

&lt;400&gt;

35  
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42

&lt;210&gt;

36

&lt;211&gt;

33

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; JH144(GCSF-forward primer)

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36  
cctctagata aaaggacccc cctgggccct gcc

33

&lt;210&gt;

37

&lt;211&gt;

28

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; JH145(GCSF-reverse primer)

&lt;400&gt;

37  
ggcagctgga tgtattttac atggggag

28

&lt;210&gt;

38

&lt;211&gt;

43

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; HY17(TFP3-LDKR-reverse primer)

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38  
gaacttgaag taggtgccct tttatcaagg atcttttcgg agc

43

&lt;210&gt;

39

&lt;211&gt;

43

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; HY18(TFP3-LDKR-forward primer)

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39  
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43

&lt;210&gt;

40

&lt;211&gt;

134

&lt;212&gt;

PRT

&lt;213&gt;

Saccharomyces cerevisiae

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(134)

&lt;223&gt; TFP3-1-1

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1 5 10 15Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr  
20 25 30

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Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr  
           35                  40                  45  
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg  
           50                  55                  60  
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala  
           65                  70                  75                  80  
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala  
                           85                  90                  95  
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser  
                   100                  105                  110  
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 Ser Cys Lys Asn Ser Gly  
           130

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 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
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 <222> (1)..(402)  
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 tgtgttgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacccttca 180  
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240  
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagg 300  
 tccgaaaaga tctcttctc tgcattctaa acattacta atgccacatc atcttctgt 360  
 gccactccat ctgtgaaaga tagctcatgt aagaattctg gt 402

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           20                  25                  30  
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr  
           35                  40                  45  
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg  
           50                  55                  60  
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala  
           65                  70                  75                  80  
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala

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85 90 95  
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser  
 100 105 110  
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 130 135 140

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 <223> TFP3-1-2

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 gctgaagggt acactccagg tgaacatgg tccaccttaa cccaaccgg ctccatctct 120  
 tgtggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180  
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240  
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagc 300  
 tccgaaaaga tctcttctct tgcatctaaa acatctacta atgccacatc atcttcttgt 360  
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 aaggacggt 429

<210> 44  
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 <223> BglII-GAP-forward primer

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<210> 45  
 <211> 26  
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 <213> Artificial Sequence

<220>  
 <223> GAP-EcoRI-reverse primer

<400> 45  
 aagaattctt gatagtgtt caattg 26